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=> s (casein kinase 1 gamma) or (casein kinase I gamma) or (CSNK1G) or (CSNK1gamma)
or (CSNK1 gamma) or (casein kinase 1, gamma) or (casein kinase I, gamma) or (CSNK1,
gamma)

L1 82 (CASEIN KINASE 1 GAMMA) OR (CASEIN KINASE I GAMMA) OR (CSNK1G)
OR (CSNK1GAMMA) OR (CSNK1 GAMMA) OR (CASEIN KINASE 1, GAMMA) OR
(CASEIN KINASE I, GAMMA) OR (CSNK1, GAMMA)

=> S p21 or CIP1 or CDKN1A or (Cyclin-dependent kinase inhibitor 1A)
L2 128374 P21 OR CIP1 OR CDKN1A OR (CYCLIN-DEPENDENT KINASE INHIBITOR 1A)

=> s l1 (P) l2
L3 4 L1 (P) L2

=> duplicate
ENTER REMOVE, IDENTIFY, ONLY, OR (?):remove
ENTER L# LIST OR (END):l3
DUPLICATE PREFERENCE IS 'EMBASE, BIOSIS, CAPLUS'
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n
PROCESSING COMPLETED FOR L3
L4 2 DUPLICATE REMOVE L3 (2 DUPLICATES REMOVED)

=> d l4 1-2 bib ab

L4 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2004:143261 CAPLUS
DN 140:176313
TI casein kinase I gamma-1 isoforms
(CSNK1G1s) as modifiers of the p21 pathway and uses thereof in
diagnosis, therapy and drug screening
IN Francis-Lang, Helen; Friedman, Lori; Kidd, Thomas; Roche, Siobhan; Zhang,
Haiguang
PA Exelixis, Inc., USA
SO PCT Int. Appl., 69 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 8

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	-----		-----	-----	-----
PI	WO 2004015071	A2	20040219	WO 2003-US24551	20030806
	WO 2004015071	A3	20040812		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,				

GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

CA 2494236	A1	20040219	CA 2003-2494236	20030806
AU 2003263995	A1	20040225	AU 2003-263995	20030806
EP 1534852	A2	20050601	EP 2003-784937	20030806

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK

JP 2005534334	T	20051117	JP 2004-527773	20030806
US 20050251870	A1	20051110	US 2005-523588	20050204

PRAI US 2002-401739P P 20020807

WO 2003-US24551 W 20030806

AB The invention has designed a dominant loss of function screen to identify genes that interact with the cyclin dependent kinase inhibitor p21 in *Drosophila*. Casein kinase I gamma-1 isoform 3 (CSNK1G1) gene was identified as a modifier of the p21 pathway. Accordingly, vertebrate orthologs of these modifiers, and preferably the human orthologs, casein kinase I gamma-1 isoform (CSNK1G1) genes are attractive drug targets for the treatment of pathologies associated with a defective p21 signaling pathway, such as cancer. The invention also provides methods for utilizing these p21 modifier genes and polypeptides to identify candidate therapeutic agents that can be used in the treatment of disorders associated with defective p21 function.

L4 ANSWER 2 OF 2 EMBASE COPYRIGHT (c) 2008 Elsevier B.V. All rights reserved on STN DUPLICATE 1

AN 1999268046 EMBASE

TI Angiotensin II stimulates serine phosphorylation of the adaptor protein Nck: Physical association with the serine/threonine kinases Pak1 and casein kinase I.

AU Voisin, Laure; Meloche, Sylvain (correspondence)

CS Centre de Recherche, Ctr. Hosp. de l'Univ. de Montreal, University of Montreal, 3850 St. Urbain, Montreal, Que. H2W 1T8, Canada. meloches@ere.umontreal.ca

AU Larose, Louise

CS Department of Experimental Medicine, McGill University, Montreal, Que. H3A 2B2, Canada.

AU Meloche, Sylvain (correspondence)

CS Centre de Recherche, Centre hospitalier Univ. de Montreal, Campus Hotel-Dieu, 3850 St. Urbain, Montreal, Que. H2W 1T8, Canada. meloches@ere.umontreal.ca

SO Biochemical Journal, (1 Jul 1999) Vol. 341, No. 1, pp. 217-223.

Refs: 44

ISSN: 0264-6021 CODEN: BIJOAK

CY United Kingdom

DT Journal; Article

FS 029 Clinical and Experimental Biochemistry

LA English

SL English

ED Entered STN: 12 Aug 1999

Last Updated on STN: 12 Aug 1999

AB Nck is a small adaptor protein consisting exclusively of three SH3 domains and one SH2 domain. Nck is thought to have an important role in cell signalling by coupling receptor tyrosine kinases, via its SH2 domain, to downstream SH3-binding effectors. We report here that angiotensin II,

working through the AT(1) receptor subtype, stimulates the phosphorylation of Nck in rat aortic smooth muscle cells. Phosphopeptide mapping analysis revealed that Nck is phosphorylated on four peptides containing exclusively phosphoserine in quiescent cells. Treatment with angiotensin II resulted in increased phosphorylation of these four peptides, without the appearance of new phosphopeptides. We show that Nck, via its SH3 domains, specifically binds three major phosphoproteins of 95, 82 and 66 kDa both in vitro and in intact cells. Notably, the phosphorylation of these Nck-binding proteins was found to increase in parallel with that of Nck on stimulation by angiotensin II. One candidate for the 66 kDa phosphoprotein is the serine/threonine kinase p21-activated kinase 1 (Pak1), which was found to form a stable complex with Nck in aortic smooth muscle cells. We have also identified the γ 2 isoform of casein kinase I as another protein kinase that associates with Nck in these cells. These findings indicate that Nck is a target of G-protein-coupled receptors and suggest a role for Pak1 and casein kinase I- γ 2 in downstream signalling or regulation of the AT(1) receptor.

=> s proliferation or (cell division) or (mitosis) or apoptosis or (cell cycle) or (meiosis) or cancer or oncogenesis

L5 4496759 PROLIFERATION OR (CELL DIVISION) OR (MITOSIS) OR APOPTOSIS OR (CELL CYCLE) OR (MEIOSIS) OR CANCER OR ONCOGENESIS

=> s l1 (P) l5

L6 23 L1 (P) L5

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DUPLICATE PREFERENCE IS 'MEDLINE, EMBASE, BIOSIS, CAPLUS'

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PROCESSING COMPLETED FOR L6

L7 10 DUPLICATE REMOVE L6 (13 DUPLICATES REMOVED)

=> d l7 1-10 bib ab

L7 ANSWER 1 OF 10 MEDLINE ON STN DUPLICATE 1
 AN 2008512208 MEDLINE
 DN PubMed ID: 18694560
 TI A casein kinase 1 and PAR proteins regulate asymmetry of a PIP(2) synthesis enzyme for asymmetric spindle positioning.
 AU Panbianco Costanza; Weinkove David; Zanin Esther; Jones David; Divecha Nallin; Gotta Monica; Ahringer Julie
 CS The Gurdon Institute and Department of Genetics, University of Cambridge, Tennis Court Road, Cambridge CB21QN, UK.
 NC 054523 (United Kingdom Wellcome Trust)
 SO Developmental cell, (2008 Aug) Vol. 15, No. 2, pp. 198-208.
 CY Journal code: 101120028. ISSN: 1534-5807.
 DT United States
 Journal; Article; (JOURNAL ARTICLE)
 (RESEARCH SUPPORT, N.I.H., EXTRAMURAL)
 (RESEARCH SUPPORT, NON-U.S. GOV'T)
 LA English
 FS Priority Journals
 EM 200809
 ED Entered STN: 13 Aug 2008
 Last Updated on STN: 7 Sep 2008
 Entered Medline: 5 Sep 2008
 AB Spindle positioning is an essential feature of asymmetric cell

division. The conserved PAR proteins together with heterotrimeric G proteins control spindle positioning in animal cells, but how these are linked is not known. In *C. elegans*, PAR protein activity leads to asymmetric spindle placement through cortical asymmetry of Galpha regulators GPR-1/2. Here, we establish that the casein kinase 1 gamma CSNK-1 and a PIP(2) synthesis enzyme (PPK-1) transduce PAR polarity to asymmetric Galpha regulation. PPK-1 is posteriorly enriched in the one-celled embryo through PAR and CSNK-1 activities. Loss of CSNK-1 causes uniformly high PPK-1 levels, high symmetric cortical levels of GPR-1/2 and LIN-5, and increased spindle pulling forces. In contrast, knockdown of ppk-1 leads to low GPR-1/2 levels and decreased spindle forces. Furthermore, loss of CSNK-1 leads to increased levels of PIP(2). We propose that asymmetric generation of PIP(2) by PPK-1 directs the posterior enrichment of GPR-1/2 and LIN-5, leading to posterior spindle displacement.

L7 ANSWER 2 OF 10 MEDLINE on STN DUPLICATE 2
AN 2006124588 MEDLINE
DN PubMed ID: 16247451
TI RNAi-based screening of the human kinome identifies Akt-cooperating kinases: a new approach to designing efficacious multitargeted kinase inhibitors.
AU Morgan-Lappe S; Woods K W; Li Q; Anderson M G; Schurdak M E; Luo Y; Giranda V L; Fesik S W; Levenson J D
CS Abbott Laboratories, Cancer Research, Abbott Park, IL 60064, USA.
SO Oncogene, (2006 Mar 2) Vol. 25, No. 9, pp. 1340-8.
Journal code: 8711562. ISSN: 0950-9232.
CY England; United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200604
ED Entered STN: 3 Mar 2006
Last Updated on STN: 19 Apr 2006
Entered Medline: 18 Apr 2006
AB Tumors comprise genetically heterogeneous cell populations, whose growth and survival depend on multiple signaling pathways. This has spurred the development of multitargeted therapies, including small molecules that can inhibit multiple kinases. A major challenge in designing such molecules is to determine which kinases to inhibit in each cancer to maximize efficacy and therapeutic index. We describe an approach to this problem implementing RNA interference technology. In order to identify Akt-cooperating kinases, we screened a library of kinase-directed small interfering RNAs (siRNAs) for enhanced cancer cell killing in the presence of Akt inhibitor A-443654. siRNAs targeting casein kinase I gamma 3 (CSNK1G3) or the inositol polyphosphate multikinase (IPMK) significantly enhanced A-443654-mediated cell killing, and caused decreases in Akt Ser-473 and ribosomal protein S6 phosphorylation. Small molecules targeting CSNK1G3 and/or IPMK in addition to Akt may thus exhibit increased efficacy and have the potential for improved therapeutic index.

L7 ANSWER 3 OF 10 MEDLINE on STN DUPLICATE 3
AN 2005658616 MEDLINE
DN PubMed ID: 16341016
TI Casein kinase 1 gamma couples Wnt receptor activation to cytoplasmic signal transduction.
AU Davidson Gary; Wu Wei; Shen Jinlong; Bilic Josipa; Fenger Ursula; Stannek Peter; Glinka Andrei; Niehrs Christof
CS Division of Molecular Embryology, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 280, D-69120 Heidelberg, Germany..

g.davidson@dkfz-heidelberg.de
 SO Nature, (2005 Dec 8) Vol. 438, No. 7069, pp. 867-72.
 Journal code: 0410462. E-ISSN: 1476-4687.
 CY England: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 (RESEARCH SUPPORT, NON-U.S. GOV'T)
 LA English
 FS Priority Journals
 OS GENBANK-DQ185136
 EM 200512
 ED Entered STN: 18 Dec 2005

Last Updated on STN: 30 Dec 2005
 Entered Medline: 29 Dec 2005
 AB Signalling by Wnt proteins (Wingless in Drosophila) has diverse roles during embryonic development and in adults, and is implicated in human diseases, including cancer. LDL-receptor-related proteins 5 and 6 (LRP5 and LRP6; Arrow in Drosophila) are key receptors required for transmission of Wnt/beta-catenin signalling in metazoa. Although the role of these receptors in Wnt signalling is well established, their coupling with the cytoplasmic signalling apparatus remains poorly defined. Using a protein modification screen for regulators of LRP6, we describe the identification of Xenopus Casein kinase 1 gamma (CK1gamma), a membrane-bound member of the CK1 family. Gain-of-function and loss-of-function experiments show that CK1gamma is both necessary and sufficient to transduce LRP6 signalling in vertebrates and Drosophila cells. In Xenopus embryos, CK1gamma is required during antero-posterior patterning to promote posteriorizing Wnt/beta-catenin signalling. CK1gamma is associated with LRP6, which has multiple, modular CK1 phosphorylation sites. Wnt treatment induces the rapid CK1gamma-mediated phosphorylation of these sites within LRP6, which, in turn, promotes the recruitment of the scaffold protein Axin. Our results reveal an evolutionarily conserved mechanism that couples Wnt receptor activation to the cytoplasmic signal transduction apparatus.

L7 ANSWER 4 OF 10 CAPLUS COPYRIGHT 2008 ACS ON STN
 AN 2004:143261 CAPLUS
 DN 140:176313
 TI casein kinase I gamma-1 isoforms (CSNK1G1s) as modifiers of the p21 pathway and uses thereof in diagnosis, therapy and drug screening
 IN Francis-Lang, Helen; Friedman, Lori; Kidd, Thomas; Roche, Siobhan; Zhang, Haiguang
 PA Exelixis, Inc., USA
 SO PCT Int. Appl., 69 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 FAN.CNT 8

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004015071	A2	20040219	WO 2003-US24551	20030806
WO 2004015071	A3	20040812		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			

CA 2494236 A1 20040219 CA 2003-2494236 20030806
AU 2003263995 A1 20040225 AU 2003-263995 20030806
EP 1534852 A2 20050601 EP 2003-784937 20030806
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK
JP 2005534334 T 20051117 JP 2004-527773 20030806
US 20050251870 A1 20051110 US 2005-523588 20050204
PRAI US 2002-401739P P 20020807
WO 2003-US24551 W 20030806
AB The invention has designed a dominant loss of function screen to identify
genes that interact with the cyclin dependent kinase inhibitor p21 in
Drosophila. Casein kinase I gamma
-1 isoform 3 (CSNK1G1) gene was identified as a modifier of the p21
pathway. Accordingly, vertebrate orthologs of these modifiers, and
preferably the human orthologs, casein kinase
I gamma-1 isoform (CSNK1G1) genes are attractive drug
targets for the treatment of pathologies associated with a defective p21
signaling pathway, such as cancer. The invention also provides
methods for utilizing these p21 modifier genes and polypeptides to
identify candidate therapeutic agents that can be used in the treatment of
disorders associated with defective p21 function.

L7 ANSWER 5 OF 10 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2004:219931 CAPLUS
DN 140:248186
TI Use of patterns of gene expression to identify tissue types and in disease
diagnosis and prognosis
IN Glinskii, Guennadi V.
PA Sidney Kimmel Cancer Center, USA
SO U.S. Pat. Appl. Publ., 209 pp., which which which which
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 20040053317	A1	20040318	US 2003-660434	20030910
	CA 2498418	A1	20040325	CA 2003-2498418	20030910
	WO 2004025258	A2	20040325	WO 2003-US28707	20030910
	WO 2004025258	A3	20050519		
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	AU 2003274970	A1	20040430	AU 2003-274970	20030910
	EP 1552293	A2	20050713	EP 2003-759240	20030910
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
	US 20050142573	A1	20050630	US 2004-861003	20040603
PRAI	US 2002-410018P	P	20020910		
	US 2002-411155P	P	20020916		
	US 2002-429168P	P	20021125		
	US 2003-444348P	P	20030131		
	US 2003-460826P	P	20030403		
	US 2003-660434	A1	20030910		

WO 2003-US28707 W 20030910

AB Methods of using quant. anal. of array hybridizations to identify normal and diseased tissue in the diagnosis and prognosis of disease are described. The methods segregate individual samples into distinct classes using quant. measurements of expression values for selected sets of genes in individual samples compared to a reference standard. Samples displaying pos. and neg. correlations of the gene expression values with the reference standard samples exhibit distinct behaviors and pathohistol. features. Also disclosed are methods for identifying sets of genes whose expression patterns are correlated with a phenotype. Such sets are useful for characterizing cellular differentiation pathways and states and for identifying potential drug discovery targets. Panels for diagnosis and determination of risk of invasive and metastatic forms of lung, prostate and breast cancer are identified. Similarly, panels indicating recurrence of the cancers and poor prognostic outcomes are identified.

L7 ANSWER 6 OF 10 MEDLINE on STN DUPLICATE 4
AN 2004279258 MEDLINE
DN PubMed ID: 15077195
TI Metastatic tumor antigen 1 short form (MTA1s) associates with casein kinase I-gamma2, an estrogen-responsive kinase.
AU Mishra Sandip K; Yang Zhibo; Mazumdar Abhijit; Talukder Amjad H; Larose Louise; Kumar Rakesh
CS Department of Molecular and Cellular Oncology, The University of Texas MD Anderson Cancer Center, Houston, TX 77030, USA.
NC CA098823 (United States NCI)
CA90970 (United States NCI)
SO Oncogene, (2004 May 27) Vol. 23, No. 25, pp. 4422-9.
Journal code: 8711562. ISSN: 0950-9232.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LA English
FS Priority Journals
EM 200407
ED Entered STN: 6 Jun 2004
Last Updated on STN: 2 Jul 2004
Entered Medline: 1 Jul 2004

AB Recent studies have shown that metastasis-associated protein-1 short form (MTA1s) - metastatic tumor antigen 1 short form sequesters estrogen receptor-alpha (ER-alpha) in the cytoplasm of breast cancer cells. Using a yeast two-hybrid screening to clone MTA1s-interacting proteins, we identified casein kinase I-gamma 2 (CKI-gamma2, a ubiquitously expressed cytoplasmic kinase) as an MTA1s-binding protein. We show that MTA1s interacts with CKI-gamma2 both in vitro and in vivo and colocalizes in the cytoplasm. In addition, we found that CKI-gamma2 can phosphorylate MTA1s, but not ER, in an antiestrogen-dependent manner and that estrogen stimulates CKI-gamma2 activity that could be effectively blocked by a specific inhibitor of CKI. CKI-gamma2 could further potentiate the ER corepressive function of MTA1s. Kinase dead CKI-gamma2 could not repress estrogen-induced ER transactivation functions. Results from mutagenesis studies suggest that substitution of the serine residue at 321 to alanine, which is a possible CKI-gamma2 phosphorylation site in MTA1s, results in a significant reduction in the ability of MTA1s to repress ER transactivation. These findings identified MTA1s as a target of CKI-gamma2, and provided new evidence to suggest that CKI-gamma2 phosphorylates and modulates the functions of MTA1s, and that these extranuclear effects of estrogen might

have important implications in regulating the functions of MTAs in human mammary epithelial and cancer cells.

L7 ANSWER 7 OF 10 CAPLUS COPYRIGHT 2008 ACS on STN

AN 2003:633500 CAPLUS

DN 139:192515

TI Proteins and genes involved in the regulation of energy homeostasis and triglyceride metabolism and their use in the diagnosis and treatment of metabolic disorders

IN Eulenberger, Karsten; Broenner, Guenter; Steuernagel, Arndt; Meise, Martin; Haeder, Thomas

PA Develogen Aktiengesellschaft Fuer Entwicklungsbiologische Forschung, Germany

SO PCT Int. Appl., 157 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003066086	A2	20030814	WO 2003-EP1094	20030204
	WO 2003066086	A3	20040122		
	W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW			
	RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
	AU 2003226973	A1	20030902	AU 2003-226973	20030204
PRAI	EP 2002-2548	A	20020204		
	EP 2002-2707	A	20020206		
	EP 2002-2891	A	20020208		
	EP 2002-3748	A	20020219		
	EP 2002-4667	A	20020228		
	EP 2002-22101	A	20021002		
	WO 2003-EP1094	W	20030204		

AB The present invention discloses casein kinase 1.γ (CSNK1G), GABAA receptor-associated protein (GABARAP), proliferation-associated 2G4 protein (PA2G4, also referred to as methionyl aminopeptidase homologous protein), molybdenum cofactor synthesis-step 1 protein (MOCS1), cell division cycle 10 protein homolog (CDC10, also referred to as septin and septin 7), pyruvate kinase (PK), calreticulin (CALR), and polynucleotides which identify and encode these proteins. These proteins are shown to be involved in the regulation of energy homeostasis, body weight regulation, and triglyceride metabolism by measuring triglyceride levels in a genetic adipose pathway screen, expression profiling, and synthesis of lipids during adipogenesis. The genetic screen demonstrates that mutations of these genes cause obesity, reflected by a significant increase of triglyceride content, the major energy storage substance. Thus, the invention relates to the use of these sequences in the diagnosis, study, prevention, and treatment of metabolic diseases and disorders.

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DUPLICATE 5

AN 2003237680 EMBASE

TI Downregulation of Cap43 gene by von Hippel-Lindau tumor suppressor protein
 in human renal cancer cells.
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 CS Department of Urology, Graduate School of Medical Sciences, Kyushu
 University, Fukuoka, Japan.
 SO International Journal of Cancer, (20 Jul 2003) Vol. 105, No. 6, pp.
 803-810.
 Refs: 38
 ISSN: 0020-7136 CODEN: IJCNAM
 CY United States
 DT Journal; Article
 FS 016 Cancer
 022 Human Genetics
 028 Urology and Nephrology
 005 General Pathology and Pathological Anatomy
 LA English
 SL English
 ED Entered STN: 3 Jul 2003
 Last Updated on STN: 3 Jul 2003
 AB We previously identified 9 genes (i.e., thymosin β 4, secreted protein
 acidic and rich in cysteine, Cap43, ceruloplasmin, serum amyloid A, heat
 shock protein 90, LOT1, osteopontin and casein kinase
 1.gamma.) that are more highly expressed in cancerous
 regions than in noncancerous regions in human renal cancers. In our
 study, we considered the possibility that the von Hippel-Lindau (VHL)
 tumor suppressor gene might be able to affect the expression of these 9
 genes in renal cancer cells. We first established 2
 VHL-positive cell lines, 786/VHL-1 and 786/VHL-2, after the introduction
 of wild-type VHL into VHL-negative renal cancer 786-0 cells. Of
 these 9 genes, expression of the Cap43 gene was specifically downregulated
 by VHL. Expression of Cap43 was also much lower in 4 other VHL-positive
 renal cancer cell lines than in VHL-negative 786-0 cells. Cap43
 promoter assays with several deletion or mutation constructs demonstrated
 that the Spl site in the element from -286 base pairs (bp) to -62 bp was
 partly responsible for VHL-induced suppression of the Cap43 gene.
 Immunostaining analysis with human specimens of renal cancers demonstrated
 that the Cap43 protein was expressed in most cancer cells and
 macrophages. We also observed a marked and specific increase of Cap43
 mRNA levels in response to hypoxia or nickel in all VHL-positive cell
 lines. Cellular expression of Cap43 mRNA in response to hypoxia or nickel
 thus is closely associated with VHL gene expression in renal
 cancer cells. Although the function of the Cap43 protein remains
 unclear, the expression of Cap43 protein could be a molecular marker
 closely associated with VHL in renal cancer. .COPYRGT. 2003
 Wiley-Liss, Inc.
 L7 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2008 ACS on STN
 AN 2003:807997 CAPLUS
 DN 140:126171
 TI Genes commonly upregulated by hypoxia in human breast cancer cells MCF-7
 and MDA-MB-231

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 CS Breast Cancer Research Group, Tokyo Metropolitan Cancer and Infectious
 Diseases Center, Bunkyo-ku, Tokyo, 113-0087, Japan
 SO Biomedicine & Pharmacotherapy (2003), 57(8), 333-340
 CODEN: BIPHEX; ISSN: 0753-3322
 PB Editions Scientifiques et Medicales Elsevier
 DT Journal
 LA English
 AB Hypoxia is a stress that causes alterations in signal transduction and
 gene instability. In the cancer microenvironment, hypoxia plays a
 significant role in forming a tumor phenotype and tumor progression. We
 aimed to identify the genes upregulated by hypoxia in human breast cancer
 cell lines, a hormone-dependent MCF-7 and a hormone-independent
 MDA-MB-231, using microarray anal. These cells were exposed to two oxygen
 concns. such as 21% and 1% in a time-course. Out of 12,625 genes, 26
 genes were identified as commonly upregulated in both MCF-7 and MDA-MB-231
 cells. Some of these genes were already reported as hypoxia-related, but
 some of those were identified newly. These commonly upregulated genes
 between hormone-dependent and hormone-independent cells would be a clue to
 study hypoxia-related events and to explore the novel therapeutic targets
 in human breast cancer.

RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 10 OF 10 CAPLUS COPYRIGHT 2008 ACS on STN
 AN 2002:440558 CAPLUS
 DN 137:260870
 TI CXCR4/CXCL12 expression and signaling in kidney cancer
 AU Schrade, A. J.; Lechner, O.; Templin, M.; Dittmar, K. E. J.; Machters,
 S.; Mengel, M.; Probst-Kepper, M.; Franzke, A.; Wollensak, T.; Gatzlaff,
 P.; Atzpodiien, J.; Buer, J.; Lauber, J.
 CS Department of Cell Biology and Immunology, German Research Centre for
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 SO British Journal of Cancer (2002), 86(8), 1250-1256
 CODEN: BJCAAI; ISSN: 0007-0920
 PB Nature Publishing Group
 DT Journal
 LA English
 AB CXCL12 (SDF-1), a CXC-chemokine, and its specific receptor, CXCR4, have
 recently been shown to be involved in tumorigenesis, proliferation and
 angiogenesis. Therefore, we analyzed CXCL12 α /CXCR4 expression and
 function in four human kidney cancer cell lines (A-498, CAKI-1, CAKI-2,
 HA-7), 10 freshly harvested human tumor samples and corresponding normal
 kidney tissue. While none of the analyzed tumor cell lines expressed
 CXCL12 α , A-498 cells were found to express CXCR4. More importantly,
 real-time RT-PCR anal. of 10 tumor samples and resp. adjacent normal
 kidney tissue disclosed a distinct and divergent downregulation of
 CXCL12 α and upregulation of CXCR4 in primary tumor tissue. To prove
 that the CXCR4 protein is functionally active, rhCXCL12 α was
 investigated for its ability to induce changes of intracellular calcium
 levels in A-498 cells. Moreover, we used cDNA expression arrays to
 evaluate the biol. influence of CXCL12 α . Comparing gene expression
 profiles in rhCXCL12 α stimulated vs. unstimulated A-498 kidney
 cancer cells revealed specific regulation of 31 out of 1176 genes tested
 on a selected human cancer array, with a prominent stimulation of genes
 involved in cell-cycle regulation and apoptosis. The genetic changes
 reported here should provide new insights into the developmental paths
 leading to tumor progression and may also aid the design of new approaches
 to therapeutic intervention.

RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

